

**Table S2.** Estimate of average pairwise genetic distance among and within five morphotypes of *B. cristata* for *trnS*-G, *ndhF*-*trnL*<sub>(UAG)</sub> and ITS region.

Morphotype name	Among morphotypes			Within morphotypes		
	Cultivated form 3	Cultivated form 2	Cultivated form 1	Nandi Hills	Uttarakhand	-
<b><i>trnS</i>-G</b>						
Cultivated form 3	-					0.0000
Cultivated form 2	0.00000	-				0.0000
Cultivated form 1	0.00000	0.00000	-			0.0000
Nandi Hills	0.00099	0.00143	0.00151	-		0.0036
Uttarakhand	0.00054	0.00081	0.00081	0.00206	-	0.0017
<b><i>ndhF</i>-<i>trnL</i><sub>(UAG)</sub></b>						
Cultivated form 3	-					0.0000
Cultivated form 2	0.000173	-				0.0004
Cultivated form 1	0.001396	0.001226	-			0.0000
Nandi Hills	0.000821	0.000915	0.002098	-		0.0003
Uttarakhand	0.001393	0.001230	0.001404	0.002135	-	0.0000
<b>ITS</b>						
Cultivated form 3	-		NA			0.0007
Cultivated form 2	0.00805	-	NA			0.0018
Nandi Hills	0.18423	0.19023	NA	-		0.0073
Uttarakhand	0.12962	0.13357	NA	0.16470	-	0.0067

**Note-** ITS sequences of cultivated form 1 morphotypes are missing. Hence, average pairwise genetic distance with remaining four morphotypes and genetic distance within morphotypes are not possible to calculate. NA- Not Applicable.